

Alpha Virus nsp3 alignment

CLUSTAL W (1.82) multiple sequence alignment

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SFV_nsp3      APSYRVKRIADIATCTEAAVVNAANARGTVGDGVCRAVAKKWPSAFKGAATPVGTIKTVMC 60
ONV_nsp3      APSYRVKRMEDIAKNTTEECVVNAANPRGVPDGVCKAVYRKWPESFRNSATPVGTAKTIMC 60
RRV_nsp3      APSYRVRRTDISGHAEAEVVNAANAKGTVGVCRAVARKWPDSFKGAATPVGTAKLVQA 60
SinV_nsp3     APSYRTKRENIADCQEEAEVVNAANPLGRPEGVCRAIYKRWPTSFTDSATETGTARMTVC 60
VEEV_nsp3     APSYHVVRGDIATATEGVIINAANSKGQPGGGVCGALYKKFPESFDLQPIEVGKARLVKG 60
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SFV_nsp3      GSYFVIHAVAPNFSATTEAEGDRELAAYRAVAEEVNRLSLSSVAIPLLSTGVFSGGRDR 120
ONV_nsp3      GQYPVIHAVGPNFNSYSEAEGDRELASVYREVAKEVSRLGVSSVAIPLLSTGVYSGGKDR 120
RRV_nsp3      NGMNVIIHAVGPNFSTVTEAEGDRELAAYRAVAGIINASNIKSVAIPLLSTGVFSGGKDR 120
SinV_nsp3     LGKKVIHAVGPDFRKHPAEALKLLQNAHAYHADLVNEHNIKSVAIPLLSTGIYAAGKDR 120
VEEV_nsp3     AAKHIIHAVGPNFNKVSEVEGDQLAEAYESIAKIVNDNNYKSVAIPLLSTGIFSGNKDR 120
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SFV_nsp3      LQQSLNHLFTAMDATDADVTIYCRDKSWEKKIQEAIDMRTAV-ELLNDD----VELTTDL 175
ONV_nsp3      LLQSLNHLFAAMDSTDADVVIYCRDKEWEKKITEAISLSQV-ELLDDH----ISVDCDI 175
RRV_nsp3      VMQSLNHLFTAMDTTDADVVIYCRDKAWEKKIQEAIDRRRTAV-ELVSED----ISLES DL 175
SinV_nsp3     LEVSLNCLTTALDRTDADVTIYCLDKKWKERIDAALQLKESVTELKDED----MEIDDEL 176
VEEV_nsp3     LTQSLNHLTLTALDTTADVAIYCRDKKWEMLTKEAVARREAVEEICISDDSSVTEPD AEL 180
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SFV_nsp3      VRVHPDSSLVGRKGYSTTDGSLYSYFEGTKFNQAAIDMAEILTLWPRQLQEANERICLYAL 235
ONV_nsp3      VRVHPDSSLAGRKGYSTVEGALYSYLEGTRFHQTAVDMAEIYTMWPKQTEANEQVCLYAL 235
RRV_nsp3      IRVHPDSCLVGRKGYSITDGKLHSYLEGTRFHQTAVDMAEISTLWPKLQDANEQICLYAL 235
SinV_nsp3     VWIHPDSCLVGRKGFSTTKGKLYSYFEGTKFHFQAAKDMAEIKVLFPNDQESNEQLCAYIL 236
VEEV_nsp3     VRVHPKSSLAGRKGYSTSDGKTFSYLEGTKFHFQAAKDIAEINAMWVPVATEANEQVCMYIL 240
              : :***.*** *****: * .*. :*: * :*: * :*: * :*: * :*: * :

SFV_nsp3      GETMDNIGSKCPVNDSDSSTPPRTVPCLCRYAMTAERIAIRLSHQVKSMMVVCSSFFLPKY 295
ONV_nsp3      GESIESVRQKCPVDDADASFPPKTVPCLCRYAMTPERVARLRMNHSTTSIIIVCSSFFLPKY 295
RRV_nsp3      GESMDSIRTKCPVEDADSSSTPPKTVPCLCRYAMTAERVARLRMNNTKAIIVCSSFFLPKY 295
SinV_nsp3     GETMEAIREKCPVDHNPSSSPKTLPCLCMYAMTPERVHRLRSNNVKEVTVCSSSTPLPKH 296
VEEV_nsp3     GESMSSIRSKCPVEESEASTPPSTLPCLCIHAMTPERVQRLKASRPEQITVCSSFFLPKY 300
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SFV_nsp3      HVDGVQKVKCEKVLFDPTVPSVSPRKYAAS-----TTDHSRSLRGFDLDWTTDSSST 350
ONV_nsp3      KIEGVQKVKCSKALLFDHNVP SRVSPRTYRPADEIIQTPQTPEACQDAQLVQSINDEAV 355
RRV_nsp3      RIEGVQKVKCDRVLIFDQTVPSLVSPRKYIPAAASMHADTVSLDSTVSTGSAWSFPSEAT 355
SinV_nsp3     KIKNVQKVQCTKVVLFPNHTPAFVPARKYIEVPE---QPTAPPAQAEAEPEVATPSPST 353
VEEV_nsp3     RITGVQKIQCSQPILFSPKVPAYIHPRKYLVTETPPVEETPESPAENQSTEGTPEQPALVN 360
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SFV_nsp3      -----ASDTMSLPSLQSCDIDSIYEPMA-----IVVTADVHP-----EPAGI 388
ONV_nsp3      PVPSDLEACDATMDWPSIGTVSTRQRHSDSDSEYSGSRSNIQLVTA DVHAPMYAHS LASS 415
RRV_nsp3      -YETMEVVAEVHHSEPPVPPRRRRRAQVTMHH-----QELLEVS DMHT-----PIAAR 402
SinV_nsp3     ADNTSLDVTDISLMDSDSSEGLFSSFSGSDN-----SITSMDSWS-----SGPSS 399
VEEV_nsp3     VDATRTRMPEPIIIIEEEEDSISLLSDGPTHQ-----VLQVEADINH-----SPSVS 407
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SFV_nsp3      ADLAADVHPEPADH-----VDLEN-----PIPPRPKRAAYLASRAAER----- 427
ONV_nsp3      GGSMLSLSSEPAQNGTMILLDSEDTSISRVTPIAPPRRLGRTINVTCDERE--GKIL 473
RRV_nsp3      VEIPVYDTAVVAER-VAIPCTSEY-----ATPIPTPRAVRVVPVPAPRIQRASTYRVS 454
SinV_nsp3     LEIVDRRQVVVADV---HAVQEP-----APIPPRLKKMARLAAARKEPTPPASNS 447
VEEV_nsp3     SSSWSIPHASDFDVDSLILDTLDG-----ASVTSGAVSAETNSYFARSMEFRAR 457
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SFV_nsp3      PVPAPR-KPTPAPRTAFR-----NKLPLTFGDGDFDEHEVDAL-- 462
ONV_nsp3      PMASDR-FFTAKPYTVALSVSTADMTVYPIQAPLGLIPPPTLEPITFGDFAEGEIDNL-- 530
RRV_nsp3      PTPTPR-VLRASVCSVTTSAG-----VEFPWAPEDLEVLTPEVHCEMREPVELFWEPE-- 506
SinV_nsp3     SESLHL-SFGGVSMSLGSI FDG---ETARQAAVQPLATGPTDVPMSFGSFS DGEIDELSR 503
VEEV_nsp3     PVPAPRTVFRNPPHPAPRTRTP----PLAHSRASSRTSLVSTPPGVNRVITREELEALTP 513
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SFV_nsp3      ---ASG-ITFGDF-----DDVRLRLGRAGA--- 482
ONV_nsp3      ---LTGALTFGDFEPGEVEELTDSEWSTCSDTDEELRLDRAGG--- 570
RRV_nsp3      ---DVD-IQFGDFET-----PDKIQFGDIDFDQF 531
SinV_nsp3     RVTSEPVLFSGFEPGEVNSIISSRSVSVFPLRKQRRRRSRTEY 549
VEEV_nsp3     SRAPSRASRTSLVS-----NPPGVNRVITREEFEAFVAQQQ-- 550
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